SEQUENCE LISTING

<110> Katherine Galvin and Laura A. Rudolph-Owen <120> METHODS AND COMPOSITIONS FOR THE DIAGNOSIS AND TREATMENT OF CARDIOVASCULAR AND TUMORIGENIC DISEASE USING 4941 <130> MPI99-283P1RCN1M <140> <141> <150> 09/635,521 <151> 2000-08-09 <150> 60/199,908 <151> 2000-04-26 <160> 3 <170> PatentIn Ver. 2.0 <210> 1 <211> 1362 <212> DNA <213> Homo sapiens <220> <221> CDS <222> (1)..(1359) atg gct tca ccc agc ctc ccg ggc agt gac tgc tcc caa atc att gat Met Ala Ser Pro Ser Leu Pro Gly Ser Asp Cys Ser Gln Ile Ile Asp 10 96 cac agt cat gtc ccc gag ttt gag gtg gcc acc tgg atc aaa atc acc His Ser His Val Pro Glu Phe Glu Val Ala Thr Trp Ile Lys Ile Thr ctt att ctg gtg tac ctg atc atc ttc gtg atg ggc ctt ctg ggg aac 144 Leu Ile Leu Val Tyr Leu Ile Ile Phe Val Met Gly Leu Leu Gly Asn 40 age gee ace att egg gte ace eag gtg etg eag aag aaa gga tae ttg 192 Ser Ala Thr Ile Arg Val Thr Gln Val Leu Gln Lys Lys Gly Tyr Leu 55 cag aag gag gtg aca gac cac atg gtg agt ttg gct tgc tcg gac atc 240 Gln Lys Glu Val Thr Asp His Met Val Ser Leu Ala Cys Ser Asp Ile 70 ttg gtg ttc ctc atc ggc atg ccc atg gag ttc tac agc atc atc tgg 288 Leu Val Phe Leu Ile Gly Met Pro Met Glu Phe Tyr Ser Ile Ile Trp 90 aat ccc ctg acc acg tcc agc tac acc ctg tcc tgc aag ctg cac act 336 Asn Pro Leu Thr Thr Ser Ser Tyr Thr Leu Ser Cys Lys Leu His Thr 100 105 tto etc tte gag gee tge age tac get aeg etg etg cac gtg etg aca

Phe	Leu	Phe 115	Glu	Ala	Cys	Ser	Туг 120	Ala	Thr	Leu	Leu	His 125	Val	Leu	Thr					
	agc Ser 130															432				
	gtg Val															480				
_	acc Thr		-	_		-	_		_	_		_	_			528				
	tac Tyr															576				
_	tcc Ser	_		_				_						_		624				
	tgt Cys 210					_	_					_		_		672				
	ggc Gly	-			_				_	_			_			720				
	tgc Cys															768				
_	gcc Ala			_			_	_	_					_	_	816				•
	agc Ser	Arg	Thr	Ala	Arg	Arg		Thr	Ile	Ile	Phe	Leu	Arg			864		. **		
	gtg Val 290												_			912				
	gct Ala		_			_		_		_						960			•	*
	tac Tyr							_		_						1008				·
	gtc Val															1056				
	gtg Val			_		_	_	-	_	_	-	_	_		-	1104				

aac ca Asn Hi 37	s Glu														1152
gcc cg Ala Ar 385			_	_	_	_						_	_		1200
tct go Ser Al															1248
gcc ga Ala Gl	_	_		_		_		_	_						1296
ccc aa Pro As									-	-					1344
cag ga Gln Gl 45	u His	_	-	tga											1362
<210><211><211><212><213>	453 PRT	sapie	ens												
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His Se	r His	Val 20	Pro	Glu	Phe	Glu	Val 25	Ala	Thr	Trp	Ile	Lys 30	Ile	Thr	
Leu Il	e Leu 35	Val	Tyr	Leu	Ile	11e 40	Phe	Val	Met	Gly	Leu 45	Leu	Gly	Asn	
Ser Al 5	a Thr 0	Ile	Arg	Val	Thr 55	Gln	Val	Leu	Gln	Lys 60 _.	Lys	Gly	Tyr	Leu	
Gln Ly	s Glu	1707													,
65		vai	Thr	Asp 70	His	Met	Val	Ser	Leu 75	Ala	Cys	Ser	Asp	11e · 80	
65 Leu Va	l Phe	Leu		70					75		_			80 Trp	
	ý.	Leu	Ile 85	70	Met	Pro	Met	Glu 90	75 Phe	Tyr	Ser	Ile	Ile 95	80 Trp	
Leu Va	o Leu	Leu Thr 100	Ile 85 Thr	70 Gly Ser	Met Ser	Pro Tyr	Met Thr 105	Glu 90 Leu	75 Phe Ser	Tyr Cys	Ser Lys	Ile Leu 110	Ile 95 His	80 Trp Thr	
Leu Va	o Leu u Phe 115 r Phe	Leu Thr 100	Ile 85 Thr	70 Gly Ser Cys	Met Ser Ser	Pro Tyr Tyr 120	Met Thr 105	Glu 90 Leu Thr	75 Phe Ser Leu	Tyr Cys Leu	Ser Lys His 125	Ile Leu 110 Val	Ile 95 His Leu	80 Trp Thr	

Val Thr Ser Ala Leu Val Ala Leu Pro Leu Leu Phe Ala Met Gly Thr Glu Tyr Pro Leu Val Asn Val Pro Ser His Arg Gly Leu Thr Cys Asn 180 185 Arg Ser Ser Thr Arg His His Glu Gln Pro Glu Thr Ser Asn Met Ser 200 Ile Cys Thr Asn Leu Ser Ser Arg Trp Thr Val Phe Gln Ser Ser Ile 210 215 Phe Gly Ala Phe Val Val Tyr Leu Val Val Leu Leu Ser Val Ala Phe 230 235 Met Cys Trp Asn Met Met Gln Val Leu Met Lys Ser Gln Lys Gly Ser Leu Ala Gly Gly Thr Arg Pro Pro Gln Leu Arg Lys Ser Glu Ser Glu Glu Ser Arg Thr Ala Arg Arg Gln Thr Ile Ile Phe Leu Arg Leu Ile Val Val Thr Leu Ala Val Cys Trp Met Pro Asn Gln Ile Arg Arg Ile Met Ala Ala Ala Lys Pro Lys His Asp Trp Thr Arg Ser Tyr Phe Arg 315 Ala Tyr Met Ile Leu Leu Pro Phe Ser Glu Thr Phe Phe Tyr Leu Ser 330 Ser Val Ile Asn Pro Leu Leu Tyr Thr Val Ser Ser Gln Gln Phe Arg Arg Val Phe Val Gln Val Leu Cys Cys Arg Leu Ser Leu Gln His Ala Asn His Glu Lys Arg Leu Arg Val His Ala His Ser Thr Thr Asp Ser Ala Arg Phe Val Gln Arg Pro Leu Leu Phe Ala Ser Arg Arg Gln Ser Ser Ala Arg Arg Thr Glu Lys Ile Phe Leu Ser Thr Phe Gln Ser Glu 410

Ala Glu Pro Gln Ser Lys Ser Gln Ser Leu Ser Leu Glu Ser Leu Glu 425

Pro Asn Ser Gly Ala Lys Pro Ala Asn Ser Ala Ala Glu Asn Gly Phe

440

435 Gln Glu His Glu Val

420

<210> 3

<211> 2528

450

<212> DNA

<213> Homo sapiens

445

<220> <221> CDS <222> (42)..(1400) <220> <223> N at positions 2490 and 2493 may be Adenine, Guanine, Cytosine or Thymine gggagtcgac ccacgcgtcc ggtagcctgg tgctctttct c atg gct tca ccc agc 56 Met Ala Ser Pro Ser ctc ccg ggc agt gac tgc tcc caa atc att gat cac agt cat gtc ccc Leu Pro Gly Ser Asp Cys Ser Gln Ile Ile Asp His Ser His Val Pro 10 gag ttt gag gtg gcc acc tgg atc aaa atc acc ctt att ctg gtg tac Glu Phe Glu Val Ala Thr Trp Ile Lys Ile Thr Leu Ile Leu Val Tyr 25 30 200 ctg atc atc ttc gtg atg ggc ctt ctg ggg aac agc gcc acc att cgg Leu Ile Ile Phe Val Met Gly Leu Leu Gly Asn Ser Ala Thr Ile Arg 40 45 gtc acc cag gtg ctg cag aag aaa gga tac ttg cag aag gag gtg aca Val Thr Gln Val Leu Gln Lys Lys Gly Tyr Leu Gln Lys Glu Val Thr 55 60 gac cac atg gtg agt ttg gct tgc tcg gac atc ttg gtg ttc ctc atc 296 Asp His Met Val Ser Leu Ala Cys Ser Asp Ile Leu Val Phe Leu Ile 70 75 ggc atg ccc atg gag ttc tac agc atc atc tgg aat ccc ctg acc acg Gly Met Pro Met Glu Phe Tyr Ser Ile Ile Trp Asn Pro Leu Thr Thr tcc agc tac acc ctg tcc tgc aag ctg cac act ttc ctc ttc gag gcc Ser Ser Tyr Thr Leu Ser Cys Lys Leu His Thr Phe Leu Phe Glu Ala 105 tgc agc tac gct acg ctg ctg cac gtg ctg aca ctc agc ttt gag cgc Cys Ser Tyr Ala Thr Leu Leu His Val Leu Thr Leu Ser Phe Glu Arg 125 120 tac atc gcc atc tgt cac ccc ttc agg tac aag gct gtg tcg gga cct Tyr Ile Ala Ile Cys His Pro Phe Arg Tyr Lys Ala Val Ser Gly Pro 135 140 536 tgc cag gtg aag ctg ctg att ggc ttc gtc tgg gtc acc tcc gcc ctg Cys Gln Val Lys Leu Leu Ile Gly Phe Val Trp Val Thr Ser Ala Leu gtg gca ctg ccc ttg ctg ttt gcc atg ggt act gag tac ccc ctg gtg 584 Val Ala Leu Pro Leu Leu Phe Ala Met Gly Thr Glu Tyr Pro Leu Val 170 175 aac gtg ccc agc cac cgg ggt ctc act tgc aac cgc tcc agc acc cgc 632

Asn Val Pro Ser His Arg Gly Leu Thr Cys Asn Arg Ser Ser Thr Arg

190

185

			_		gag Glu				-			_				680
	_	_			gtg Val		-		-				_			728
_				_	ctg Leu 235			_	_		_	_			-	776
-	_			_	aaa Lys	_	-	-		_	-	-			_	824
		-	_	_	agg Arg	_			_	-		-			_	872
					atc Ile		_		_		-			_	_	920
_	_		_		aac Asn	_					_	_		_		968
	_		_		acg Thr 315	-					_		_			1016
					acg Thr											1064
	_		-		tcc Ser	_	_	_							_	1112
	_	_	_	-	ctg Leu	_	_	_		_				_	_	1160
				-	cac His				-			_			_	1208
	_	-			gcg Ala 395			-	_	• -		-		_		1256
					agc Ser			_	_		-	_		_		1304
		_		_	agt Ser											1352
					gct Ala											1400

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